

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/561,040
Source: FWP
Date Processed by STIC: 12/6/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 12/06/2006

PATENT APPLICATION: US/10/561,040

TIME: 10:10:57

Input Set : A:\P28994.APP

Output Set : N:\CRF4\12062006\J561040.raw

```

3 <110> APPLICANT: MIYAWAKI, ATSUSHI
4     TSUTSUI, HIDEKAZU
5     KARASAWA, SATOSHI
7 <120> TITLE OF INVENTION: FLUORESCENT PROTEIN
9 <130> FILE REFERENCE: P28994
11 <140> CURRENT APPLICATION NUMBER: 10/561,040
12 <141> CURRENT FILING DATE: 2005-12-16
14 <150> PRIOR APPLICATION NUMBER: PCT/JP04/08790
15 <151> PRIOR FILING DATE: 2004-06-16
17 <150> PRIOR APPLICATION NUMBER: JP 2003-170330
18 <151> PRIOR FILING DATE: 2003-06-16
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 227
26 <212> TYPE: PRT
27 <213> ORGANISM: Favia fавus
29 <400> SEQUENCE: 1
30 Met Ser Val Ile Thr Ser Glu Met Lys Met Glu Leu Leu Met Glu Gly
31 1 5 10 15
33 Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
34 20 25 30
36 Pro Phe Glu Gly Ile Gln Asn Met Asp Leu Thr Val Ile Glu Gly Gly
37 35 40 45
39 Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Val Phe Asp Tyr Gly
40 50 55 60
42 Asn Arg Val Phe Val Lys Tyr Pro Glu Glu Ile Val Asp Tyr Phe Lys
43 65 70 75 80
45 Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr Glu
46 85 90 95
48 Asp Gly Gly Ile Cys Leu Ala Thr Asn Asn Ile Thr Met Lys Lys Asp
49 100 105 110
51 Gly Ser Asn Cys Phe Val Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe
52 115 120 125
54 Pro Ala Asn Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
55 130 135 140
57 Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val
58 145 150 155 160
60 Asn Met Ala Leu Leu Leu Gln Gly Gly Gly His Tyr Arg Cys Asp Phe
61 165 170 175
63 Arg Thr Thr Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His
64 180 185 190
66 Phe Val Asp His Arg Ile Glu Ile Thr Ser His Asp Lys Asp Tyr Asn

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67          195          200          205
69 Lys Val Lys Leu Tyr Glu His Ala Lys Ala His Ser Gly Leu Pro Arg
70          210          215          220
72 Leu Ala Lys
73 225
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 684
78 <212> TYPE: DNA
79 <213> ORGANISM: Favia favius
81 <220> FEATURE:
82 <221> NAME/KEY: CDS
83 <222> LOCATION: (1)..(681)
85 <400> SEQUENCE: 2
86 atg agt gtg att aca tca gaa atg aag atg gag ctg ctt atg gaa ggc 48
87 Met Ser Val Ile Thr Ser Glu Met Lys Met Glu Leu Leu Met Glu Gly
88 1 5 10 15
90 gct gta aac ggg cac aag ttc gtg att aca ggg aaa gga agt ggc cag 96
91 Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
92 20 25 30
94 cct ttc gag gga ata cag aat atg gac ctg aca gtc ata gag ggc gga 144
95 Pro Phe Glu Gly Ile Gln Asn Met Asp Leu Thr Val Ile Glu Gly Gly
96 35 40 45
98 cct ctt cct ttt gct ttc gat atc ctg aca aca gta ttc gat tac ggc 192
99 Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Val Phe Asp Tyr Gly
100 50 55 60
102 aac cgg gta ttt gtc aaa tac cca gaa gaa ata gta gac tac ttc aag 240
103 Asn Arg Val Phe Val Lys Tyr Pro Glu Glu Ile Val Asp Tyr Phe Lys
104 65 70 75 80
106 cag tcg ttt cct gag ggt tat tct tgg gaa cga agc atg agt tac gaa 288
107 Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr Glu
108 85 90 95
110 gac ggg gga att tgc ctc gcc aca aac aat ata acg atg aag aaa gac 336
111 Asp Gly Gly Ile Cys Leu Ala Thr Asn Asn Ile Thr Met Lys Lys Asp
112 100 105 110
114 ggc agc aac tgt ttt gtc tat gaa att cga ttt gat ggt gtg aac ttt 384
115 Gly Ser Asn Cys Phe Val Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe
116 115 120 125
118 cct gcc aat ggt cca gtt atg cag agg aag acc gtc aaa tgg gag cca 432
119 Pro Ala Asn Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
120 130 135 140
122 tcc act gag aaa atg tat gtg cgt gat gga gtg ctg aag ggt gat gtt 480
123 Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val
124 145 150 155 160
126 aac atg gct ctg ttg ctt caa gga ggt ggc cat tac cga tgt gac ttc 528
127 Asn Met Ala Leu Leu Leu Gln Gly Gly Gly His Tyr Arg Cys Asp Phe
128 165 170 175
130 aga act act tac aaa gca aag aag gtt gtc cag ttg cca gac tat cac 576
131 Arg Thr Thr Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His
132 180 185 190

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134 ttc gtg gat cat cga att gag ata aca agc cat gac aag gat tac aac      624
135 Phe Val Asp His Arg Ile Glu Ile Thr Ser His Asp Lys Asp Tyr Asn
136      195      200      205
138 aag gtt aag ctg tat gag cat gct aaa gct cat tcc ggg ctg cca agg      672
139 Lys Val Lys Leu Tyr Glu His Ala Lys Ala His Ser Gly Leu Pro Arg
140      210      215      220
142 ctg gcc aag taa      684
143 Leu Ala Lys
144 225
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 23
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
154     primer
156 <220> FEATURE:
157 <221> NAME/KEY: modified_base
158 <222> LOCATION: (3)
159 <223> OTHER INFORMATION: Inosine
161 <220> FEATURE:
162 <221> NAME/KEY: modified_base
163 <222> LOCATION: (9)
164 <223> OTHER INFORMATION: Inosine
166 <220> FEATURE:
167 <221> NAME/KEY: modified_base
168 <222> LOCATION: (21)
169 <223> OTHER INFORMATION: a, c, g, t, unknown or other
171 <400> SEQUENCE: 3
W--> 172 ggnwsbgtna ayggvcayda ntt      23
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 27
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
182     primer
184 <400> SEQUENCE: 4
185 aactggaaga attcgcggcc gcaggaa      27
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 23
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
195     primer
197 <220> FEATURE:
198 <221> NAME/KEY: modified_base
199 <222> LOCATION: (11)

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200 <223> OTHER INFORMATION: Inosine
202 <220> FEATURE:
203 <221> NAME/KEY: modified_base
204 <222> LOCATION: (14)
205 <223> OTHER INFORMATION: Inosine
207 <220> FEATURE:
208 <221> NAME/KEY: modified_base
209 <222> LOCATION: (20)
210 <223> OTHER INFORMATION: Inosine
212 <400> SEQUENCE: 5
W--> 213 tgccwtttgc nttn gayatn ttg 23
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 35
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
223     primer
225 <220> FEATURE:
226 <221> NAME/KEY: modified_base
227 <222> LOCATION: (4)
228 <223> OTHER INFORMATION: Inosine
230 <220> FEATURE:
231 <221> NAME/KEY: modified_base
232 <222> LOCATION: (15)
233 <223> OTHER INFORMATION: Inosine
235 <220> FEATURE:
236 <221> NAME/KEY: modified_base
237 <222> LOCATION: (18)
238 <223> OTHER INFORMATION: Inosine
240 <220> FEATURE:
241 <221> NAME/KEY: modified_base
242 <222> LOCATION: (21)
243 <223> OTHER INFORMATION: Inosine
245 <400> SEQUENCE: 6
W--> 246 gtcntcttyt gcacnacngg nccatydgva ggaaa 35
249 <210> SEQ ID NO: 7
250 <211> LENGTH: 36
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
256     primer
258 <220> FEATURE:
259 <221> NAME/KEY: modified_base
260 <222> LOCATION: (24)..(25)
261 <223> OTHER INFORMATION: Inosine
263 <220> FEATURE:
264 <221> NAME/KEY: modified_base

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RAW SEQUENCE LISTING

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Input Set : A:\P28994.APP

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265 <222> LOCATION: (29)..(30)  /
266 <223> OTHER INFORMATION: Inosine
268 <220> FEATURE:
269 <221> NAME/KEY: modified_base
270 <222> LOCATION: (34)..(35)  /
271 <223> OTHER INFORMATION: Inosine
273 <400> SEQUENCE: 7
W--> 274 ggccacgcgt cgactagtac gggngggggn gggngg          36
277 <210> SEQ ID NO: 8
278 <211> LENGTH: 30
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
284     primer
286 <400> SEQUENCE: 8
287 ttgtcaagat atcgaaagcg aacggcagag          30
290 <210> SEQ ID NO: 9
291 <211> LENGTH: 20
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
297     primer
299 <400> SEQUENCE: 9
300 ggccacgcgt cgactagtac          20
303 <210> SEQ ID NO: 10
304 <211> LENGTH: 30
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
310     primer
312 <400> SEQUENCE: 10
313 gtccaccctc tacgactttg agttccatat          30
316 <210> SEQ ID NO: 11
317 <211> LENGTH: 44
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
323     primer
325 <400> SEQUENCE: 11
326 cccgatccg atgagtgatga ttacawcaga aatgaagatg gagg          44
329 <210> SEQ ID NO: 12
330 <211> LENGTH: 227
331 <212> TYPE: PRT
332 <213> ORGANISM: Favia favius
334 <400> SEQUENCE: 12

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/561,040

DATE: 12/06/2006
TIME: 10:10:58

Input Set : A:\P28994.APP
Output Set: N:\CRF4\12062006\J561040.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3, 9, 21
Seq#:5; N Pos. 11, 14, 20
Seq#:6; N Pos. 4, 15, 18, 21
Seq#:7; N Pos. 24, 25, 29, 30, 34, 35

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/561,040**

DATE: 12/06/2006

TIME: 10:10:58

Input Set : **A:\P28994.APP**

Output Set: **N:\CRF4\12062006\J561040.raw**

L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0